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SEQUENCE LISTING

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<120> A NOVEL ANDROGEN-INDUCED SUPPRESSOR OF CELL
PROLIFERATION AND USES THEREOF

<130> MBI-008

<140> US 09/512,581
<141> 2000-02-24

<150> US 60/121,461
<151> 1999-02-24

<160> 6

<170> PatentIn Ver. 2.0

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Ala Ser Asp Phe Leu Lys His Pro Gly Lys Asp Val Arg Leu Leu
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Pro Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr
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His Asp Val Ile Val Ser Ile Val Thr Ala Ala Lys Lys Asp Ile Leu			
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Tyr Lys Tyr Ala Leu Gln Ser Ala Ala Gly Lys Asp Ala Ala Lys			
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Gln Ile Ala Trp Ile Lys Asp Lys Leu Leu His Ile Tyr Tyr Gln Asn			
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Lys Val Met Val Ile Thr Arg Asn Leu Pro Asp Pro Gly Lys Ala Gln			
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Arg Lys Gln Leu Glu Val Leu Val Ser Pro Thr Cys Ser Cys Lys Gln			
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Gln Pro Thr Asn Pro Phe Leu	Glu Met Ile Lys Phe Leu Leu Glu Arg		
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Leu Ser Phe Thr His Pro Ile Ser Phe His Ser Ala Glu Thr Phe Glu			
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675	680	685	
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Ala Leu Gln Ile Phe Lys Asn Thr Gly Ser Lys Ile Glu Glu Asp Phe			
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Pro His Ile Arg Ser Ala Leu Leu Pro Val Leu His His Lys Ser Lys			
705	710	715	
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Val Thr Ile Gly His Ile Ala Leu Leu Ala Pro Asp Gln Phe Ala Ala			
770	775	780	
cct tgg aaa tct tgg gta gct act ttc att gtg aaa gat ctt ctc atg		2462	
Pro Trp Lys Ser Trp Val Ala Thr Phe Ile Val Lys Asp Leu Leu Met			
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Met Val Arg Trp Leu Leu Gly Met Lys Asn Asn His Ser Lys Ser Gly			

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Ser Asp Phe Phe Leu Lys His Pro Gly Lys Asp Val Arg Leu Leu Val
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Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala Pro
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Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr Arg
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325 330 335

Ala Ser His Cys Leu Met Asn His Pro Asp Leu Ala Lys Asp Leu Thr
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Glu Tyr Leu Lys Val Arg Ser His Asp Pro Glu Glu Ala Ile Arg His
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Asp Val Ile Val Ser Ile Val Thr Ala Ala Lys Lys Asp Ile Leu Leu
370 375 380

Val Asn Asp His Leu Leu Asn Phe Val Arg Glu Arg Thr Leu Asp Lys
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405 410 415

Lys Lys Tyr Ala Leu Gln Ser Ala Ala Gly Lys Asp Ala Ala Lys Gln
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Ile Ala Trp Ile Lys Asp Lys Leu Leu His Ile Tyr Tyr Gln Asn Ser
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625 630 635 640

Pro Thr Asp Gln Ala Ile Arg Ala Gly Leu Glu Leu Leu Lys Val Leu
645 650 655

Ser Phe Thr His Pro Ile Ser Phe His Ser Ala Glu Thr Phe Glu Ser
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Leu Leu Ala Cys Leu Lys Met Asp Asp Glu Lys Val Ala Glu Ala Ala
675 680 685

Leu Gln Ile Phe Lys Asn Thr Gly Ser Lys Ile Glu Glu Asp Phe Pro
690 695 700

His Ile Arg Ser Ala Leu Leu Pro Val Leu His His Lys Ser Lys Lys
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Gly Pro Pro Arg Gln Ala Lys Tyr Ala Ile His Cys Ile His Ala Ile
725 730 735

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Ala Ala Val Ser Glu Lys Leu Leu Ser Leu Leu Pro Glu Tyr Val Val

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Pro Tyr Thr Ile His Leu Leu Ala His Asp Pro Asp Tyr Val Lys Val
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Gln Asp Ile Glu Gln Leu Lys Asp Val Lys Glu Cys Leu Trp Phe Val
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 Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met Val
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 Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln Asp
 35 40 45

tct gaa gaa gaa aag gag ctt tat tta aac cta gct tta cat ctt gct 192
 Ser Glu Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu Ala
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tca gat ttt ttt ctc aag cat cct ggt aaa gat gtt cgc tta ctg gta 240
 Ser Asp Phe Phe Leu Lys His Pro Gly Lys Asp Val Arg Leu Leu Val
 65 70 75 80

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 Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala Pro
 85 90 95

tac aca tcc cct gat aaa cta aag gat ata ttt atg ttt ata aca aga 336
 Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr Arg
 100 105 110

cag ttg aag ggg cta gag gat aca aag agc cca caa ttc aat agg tat 384
 Gln Leu Lys Gly Leu Glu Asp Thr Lys Ser Pro Gln Phe Asn Arg Tyr
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 Phe Tyr Leu Leu Glu Asn Ile Ala Trp Val Lys Ser Tyr Asn Ile Cys

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cag gag ctt ttg gat acg gtt tta gta aat ctg gta cct gct cat aag Gln Glu Leu Leu Asp Thr Val Leu Val Asn Leu Val Pro Ala His Lys 195 200 205			624
aat tta aac aag caa gca tat gat ttg gca aag gct tta ctg aag agg Asn Leu Asn Lys Gln Ala Tyr Asp Leu Ala Lys Ala Leu Leu Lys Arg 210 215 220			672
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gag tat ctt aaa gtg agg tca cat gac cct gag gaa gct att aga cat Glu Tyr Leu Lys Val Arg Ser His Asp Pro Glu Glu Ala Ile Arg His 355 360 365			1104
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 Val Asn Asp His Leu Leu Asn Phe Val Arg Glu Arg Thr Leu Asp Lys
 385 390 395 400

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 Phe Met Lys Lys Phe Thr Gln Val Leu Glu Asp Asp Glu Lys Ile Arg
 545 550 555 560

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 Lys Gln Leu Glu Val Leu Val Ser Pro Thr Cys Ser Cys Lys Gln Ala
 565 570 575

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 Glu Gly Cys Val Arg Glu Ile Thr Lys Lys Leu Gly Asn Pro Lys Gln
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 Pro Thr Asn Pro Phe Leu Glu Met Ile Lys Phe Leu Leu Glu Arg Ile
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Glu Ile Ile Thr Leu Glu Gln Tyr Gln Leu Cys Ala Leu Ala Ile Asn			
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Asp Glu Cys Tyr Gln Val Arg Gln Val Phe Ala Gln Lys Leu His Lys			
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Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg Ala His Ala Arg Gln			
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Cys Leu Val Lys Asn Ile Asn Val Arg Arg Glu Tyr Leu Lys Gln His			
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Gln Asp Ile Glu Gln Leu Lys Asp Val Lys Glu Cys Leu Trp Phe Val			
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Phe Ser Asn Thr Lys Asn Tyr Leu Pro Pro Glu Met Lys Ser Phe Phe			

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1300	1305	1310		
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1315	1320	1325		
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Thr Phe Met Asp Met Asp Gln Asp Ser Glu Glu Glu Lys Glu Leu Tyr
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90 95 100

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Lys Ser Pro Gln Phe Asn Arg Tyr Phe Tyr Leu Leu Glu Asn Ile Ala
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Trp Val Lys Ser Tyr Asn Ile Cys Phe Glu Leu Glu Asp Ser Asn Glu																																																																																																																							
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150																																																																																																																							
att ttc acc cag cta tac aga acc tta ttt tca gtt ata aac aat ggc	653																																																																																																																						
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155	160	165		cac aat cag aaa gtc cat atg cac atg gta gac ctt atg agc tct att	701	His Asn Gln Lys Val His Met His Met Val Asp Leu Met Ser Ser Ile		170	175	180		att tgt gaa ggt gat aca gtg tct cag gag ctt ttg gat acg gtt tta	749	Ile Cys Glu Gly Asp Thr Val Ser Gln Glu Leu Leu Asp Thr Val Leu		185	190	195	200	gta aat ctg gta cct got cat aag aat tta aac aag caa gca tat gat	797	Val Asn Leu Val Pro Ala His Lys Asn Leu Asn Lys Gln Ala Tyr Asp		205	210	215		ttg gca aag gct tta ctg aag agg aca gct caa gct att gag cca tat	845	Leu Ala Lys Ala Leu Leu Lys Arg Thr Ala Gln Ala Ile Glu Pro Tyr		220	225	230		att acc act ttt ttt aat cag ctt ctg atg ctt ggg aaa aca tct atc	893	Ile Thr Thr Phe Phe Asn Gln Val Leu Met Leu Gly Lys Thr Ser Ile		235	240	245		agc gat ttg tca gag cat gtc ttt gac tta att ttg gag ctc tac aat	941	Ser Asp Leu Ser Glu His Val Phe Asp Leu Ile Leu Glu Leu Tyr Asn		250	255	260		att gat agt cat ttg ctg ctc tct gtt tta ccc cag ctt gaa ttt aaa	989	Ile Asp Ser His Leu Leu Leu Ser Val Leu Pro Gln Leu Glu Phe Lys		265	270	275	280	tta aag agc aat gat aat gag gag cgc cta caa gtt gtt aaa cta ctg	1037	Leu Lys Ser Asn Asp Asn Glu Glu Arg Leu Gln Val Val Lys Leu Leu		285	290	295		gca aaa atg ttt ggg gca aag gat tca gaa ttg gct tct caa aac aag	1085	Ala Lys Met Phe Gly Ala Lys Asp Ser Glu Leu Ala Ser Gln Asn Lys		300	305	310		cca ctt tgg cag tgc tac ttg ggc agg ttt aat gat atc cat gta cca	1133	Pro Leu Trp Gln Cys Tyr Leu Gly Arg Phe Asn Asp Ile His Val Pro		315	320	325		atc cgc ctg gaa tgt gtg aaa ttt gct agc cat tgt ctc atg aac cat	1181	Ile Arg Leu Glu Cys Val Lys Phe Ala Ser His Cys Leu Met Asn His		330	335	340		cct gat tta gca aaa gac tta aca gag tat ctt aaa gtg agg tca cat	1229	Pro Asp Leu Ala Lys Asp Leu Thr Glu Tyr Leu Lys Val Arg Ser His		345	350	355	360	gac cct gag gaa gct att aga cat gat gtt att gtg tca ata gtt aca	1277	Asp Pro Glu Glu Ala Ile Arg His Asp Val Ile Val Ser Ile Val Thr		365	370	375		gct gct aaa aag gat att ctt ctg gtc aat gat cac tta ctt aat ttt	1325	Ala Ala Lys Lys Asp Ile Leu Leu Val Asn Asp His Leu Leu Asn Phe									
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345	350	355	360	gac cct gag gaa gct att aga cat gat gtt att gtg tca ata gtt aca	1277	Asp Pro Glu Glu Ala Ile Arg His Asp Val Ile Val Ser Ile Val Thr		365	370	375		gct gct aaa aag gat att ctt ctg gtc aat gat cac tta ctt aat ttt	1325	Ala Ala Lys Lys Asp Ile Leu Leu Val Asn Asp His Leu Leu Asn Phe																																																																																																									
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gac cct gag gaa gct att aga cat gat gtt att gtg tca ata gtt aca	1277																																																																																																																						
Asp Pro Glu Glu Ala Ile Arg His Asp Val Ile Val Ser Ile Val Thr																																																																																																																							
365	370	375		gct gct aaa aag gat att ctt ctg gtc aat gat cac tta ctt aat ttt	1325	Ala Ala Lys Lys Asp Ile Leu Leu Val Asn Asp His Leu Leu Asn Phe																																																																																																																	
375																																																																																																																							
gct gct aaa aag gat att ctt ctg gtc aat gat cac tta ctt aat ttt	1325																																																																																																																						
Ala Ala Lys Lys Asp Ile Leu Leu Val Asn Asp His Leu Leu Asn Phe																																																																																																																							

380	385	390	
gtg aga gag aga aca tta gac aaa cga tgg aga gta cgc aaa gaa gcc Val Arg Glu Arg Thr Leu Asp Lys Arg Trp Arg Val Arg Lys Glu Ala 395	400	405	1373
atg atg gga ctt gcc caa att tat aag aaa tat gct tta cag tca gca Met Met Gly Ile Ala Gln Ile Tyr Lys Tyr Ala Leu Gln Ser Ala 410	415	420	1421
gct gga aaa gat gct gca aaa cag ata gca tgg atc aaa gac aaa ttg Ala Gly Lys Asp Ala Ala Lys Gln Ile Ala Trp Ile Lys Asp Lys Leu 425	430	435	1469
cta cat ata tat tat caa aat agt att gat gat cga cta ctt gtt gaa Leu His Ile Tyr Tyr Gln Asn Ser Ile Asp Asp Arg Leu Leu Val Glu 445	450	455	1517
cgg atc ttt gct caa tac atg gtt cct cac aat tta gaa act aca gaa Arg Ile Phe Ala Gln Tyr Met Val Pro His Asn Leu Glu Thr Thr Glu 460	465	470	1565
cgg atg aaa tgc tta tat tac ttg tat gcc aca ctg gat tta aat gct Arg Met Lys Cys Leu Tyr Tyr Leu Tyr Ala Thr Leu Asp Leu Asn Ala 475	480	485	1613
gtg aaa gca ttg aat gaa atg tgg aaa tgt caa aat ctg ctc cga cat Val Lys Ala Leu Asn Glu Met Trp Lys Cys Gln Asn Leu Leu Arg His 490	495	500	1661
caa gta aag gat ttg ctt gac ttg att aag caa ccc aaa aca gat gcc Gln Val Lys Asp Leu Leu Asp Leu Ile Lys Gln Pro Lys Thr Asp Ala 505	510	515	1709
agt gtc aag gcc ata ttt tca aaa gtg atg gtt att aca aga aat tta Ser Val Lys Ala Ile Phe Ser Lys Val Met Val Ile Thr Arg Asn Leu 525	530	535	1757
cct gat cct ggt aag gct cag gat ttc atg aag aaa ttc aca cag gtg Pro Asp Pro Gly Lys Ala Gln Asp Phe Met Lys Lys Phe Thr Gln Val 540	545	550	1805
tta gaa gat gat gag aaa ata aga aag cag tta gaa gta ctt gtt agt Leu Glu Asp Asp Glu Lys Ile Arg Lys Gln Leu Glu Val Leu Val Ser 555	560	565	1853
cca aca tgc tcc tgc aag cag gct gaa ggt tgt gtg cgt gaa ata act Pro Thr Cys Ser Cys Lys Gln Ala Glu Gly Cys Val Arg Glu Ile Thr 570	575	580	1901
aag aag ttg ggc aac ccc aaa cag cct aca aat cct ttc ctg gaa atg Lys Lys Leu Gly Asn Pro Lys Gln Pro Thr Asn Pro Phe Leu Glu Met 585	590	595	1949
atc aag ttt ctc ttg gag agg ata gca cct gtg cac ata gat acc gaa Ile Lys Phe Leu Leu Glu Arg Ile Ala Pro Val His Ile Asp Thr Glu 605	610	615	1997
tct atc agt gct ctt att aaa caa gtg aac aaa tca ata gat gga aca Ser Ile Ser Ala Leu Ile Lys Gln Val Asn Lys Ser Ile Asp Gly Thr 620	625	630	2045

gca gat gat gaa gat gag ggt gtt cca act gat caa gcc atc aga gca Ala Asp Asp Glu Asp Glu Gly Val Pro Thr Asp Gln Ala Ile Arg Ala 635 640 645	2093
ggt ctt gaa ctg ctt aag gta ctc tca ttt aca cat ccc atc tca ttt Gly Leu Glu Leu Leu Lys Val Leu Ser Phe Thr His Pro Ile Ser Phe 650 655 660	2141
cat tct gct gaa aca ttt gaa tca tta ctg gct tgt ctg aaa atg gat His Ser Ala Glu Thr Phe Glu Ser Leu Leu Ala Cys Leu Lys Met Asp 665 670 675 680	2189
gat gaa aaa gta gca gaa gct gca cta caa att ttc aaa aac aca gga Asp Glu Lys Val Ala Glu Ala Leu Gln Ile Phe Lys Asn Thr Gly 685 690 695	2237
agc aaa att gaa gag gat ttt cca cac atc aga tca gcc ttg ctt cct Ser Lys Ile Glu Glu Asp Phe Pro His Ile Arg Ser Ala Leu Leu Pro 700 705 710	2285
gtt tta cat cac aaa tct aaa aaa gga ccc ccc cgt caa gcc aaa tat Val Leu His His Lys Ser Lys Lys Gly Pro Pro Arg Gln Ala Lys Tyr 715 720 725	2333
gcc att cat tgt atc cat gcg ata ttt tct agt aaa gag acc cag ttt Ala Ile His Cys Ile His Ala Ile Phe Ser Ser Lys Glu Thr Gln Phe 730 735 740	2381
gca cag ata ttt gag cct ctg cat aag agc cta gat cca agc aac ctg Ala Gln Ile Phe Glu Pro Leu His Lys Ser Leu Asp Pro Ser Asn Leu 745 750 755 760	2429
gaa cat ctc ata aca cca ttg gtt act att ggt cat att gct ctc ctt Glu His Leu Ile Thr Pro Leu Val Thr Ile Gly His Ile Ala Leu Leu 765 770 775	2477
gca cct gat caa ttt gct gct cct tgg aaa tct tgg gta gct act ttc Ala Pro Asp Gln Phe Ala Ala Pro Trp Lys Ser Trp Val Ala Thr Phe 780 785 790	2525
att gtg aaa gat ctt ctc atg aat gat cgg ctt cca ggg aaa aag aca Ile Val Lys Asp Leu Leu Met Asn Asp Arg Leu Pro Gly Lys Lys Thr 795 800 805	2573
act aaa ctt tgg gtt cca gat gaa gaa gta tct cct gag aca atg gtc Thr Lys Leu Trp Val Pro Asp Glu Glu Val Ser Pro Glu Thr Met Val 810 815 820	2621
aaa att cag gct att aaa atg atg gtt cga tgg cta ctt gga atg aaa Lys Ile Gln Ala Ile Lys Met Met Val Arg Trp Leu Leu Gly Met Lys 825 830 835 840	2669
aat aat cac agt aaa tca gga act tct acc tta aga ttg cta aca aca Asn Asn His Ser Lys Ser Gly Thr Ser Thr Leu Arg Leu Leu Thr Thr 845 850 855	2717
ata ttg cat agt gat gga gac ttg aca gaa cag ggg aaa att agt aaa Ile Leu His Ser Asp Gly Asp Leu Thr Glu Gln Gly Lys Ile Ser Lys 860 865 870	2765

cca gat atg tca cgt ctg aga ctt gct gct ggg agt gct att gtg aag Pro Asp Met Ser Arg Leu Arg Leu Ala Ala Gly Ser Ala Ile Val Lys 875 880 885	2813
ctg gca caa gaa ccc tgt tac cat gaa atc atc aca tta gaa caa tat Leu Ala Gln Glu Pro Cys Tyr His Glu Ile Ile Thr Leu Glu Gln Tyr 890 895 900	2861
cag cta tgt gca tta gct atc aac gat gaa tgc tat caa gta aga caa Gln Leu Cys Ala Leu Ala Ile Asn Asp Glu Cys Tyr Gln Val Arg Gln 905 910 915 920	2909
gtg ttt gcc cag aaa ctt cac aaa ggc ctt tcc cgt tta cg g ctt cca Val Phe Ala Gln Lys Leu His Lys Gly Leu Ser Arg Leu Arg Leu Pro 925 930 935	2957
ctt gag tat atg gca atc tgt g cc ctt tgt gca aaa gat cct gta aag Leu Glu Tyr Met Ala Ile Cys Ala Leu Cys Ala Lys Asp Pro Val Lys 940 945 950	3005
gag aga aga gct cat gct agg caa tgt ttg gtg aaa aat ata aat gta Glu Arg Arg Ala His Ala Arg Gln Cys Leu Val Lys Asn Ile Asn Val 955 960 965	3053
agg cgg gag tat ctg aag cag cat gca gct gtt agt gaa aaa tta ttg Arg Arg Glu Tyr Leu Lys Gln His Ala Ala Val Ser Glu Lys Leu Leu 970 975 980	3101
tct ctt cta cca gag tat gtt gtt cca tat aca att cac ctt ttg gca Ser Leu Leu Pro Glu Tyr Val Val Pro Tyr Thr Ile His Leu Leu Ala 985 990 995 1000	3149
cat gac cca gat tat gtc aaa gta cag gat att gaa caa ctt aaa gat His Asp Pro Asp Tyr Val Lys Val Gln Asp Ile Glu Gln Leu Lys Asp 1005 1010 1015	3197
gtt aaa gaa tgt ctt tgg ttt gtt ctg gaa ata tta atg gct aaa aat Val Lys Glu Cys Leu Trp Phe Val Leu Glu Ile Leu Met Ala Lys Asn 1020 1025 1030	3245
gaa aat aac agt cac gct ttt atc aga aag atg gta gaa aat att aaa Glu Asn Asn Ser His Ala Phe Ile Arg Lys Met Val Glu Asn Ile Lys 1035 1040 1045	3293
caa aca aaa gat gcc caa gga cca gat gat gca aaa atg aat gaa aaa Gln Thr Lys Asp Ala Gln Gly Pro Asp Asp Ala Lys Met Asn Glu Lys 1050 1055 1060	3341
ctg tac act gtg tgt gat gtt gcc atg aat atc atc atg tca aag agt Leu Tyr Thr Val Cys Asp Val Ala Met Asn Ile Ile Met Ser Lys Ser 1065 1070 1075 1080	3389
act aca tac agt ttg gaa tct cct aaa gac ccg gta cta cca gct cgt Thr Thr Tyr Ser Leu Glu Ser Pro Lys Asp Pro Val Leu Pro Ala Arg 1085 1090 1095	3437
ttc ttc act caa cct gac aag aat ttc agt aac acc aaa aat tat ctg Phe Phe Thr Gln Pro Asp Lys Asn Phe Ser Asn Thr Lys Asn Tyr Leu 1100 1105 1110	3485
cct cct gaa atg aaa tca ttt ttc act cct gga aaa cct aaa aca acc	3533

Pro Pro Glu Met Lys Ser Phe Phe Thr Pro Gly Lys Pro Lys Thr Thr			
1115	1120	1125	
aat gtt cta gga gct gtt aac aag cca ctt tca tca gca ggc aag caa			3581
Asn Val Leu Gly Ala Val Asn Lys Pro Leu Ser Ser Ala Gly Lys Gln			
1130	1135	1140	
tct cag acc aaa tca tca cga atg gaa act gta agc aat gca agc agc			3629
Ser Gln Thr Lys Ser Ser Arg Met Glu Thr Val Ser Asn Ala Ser Ser			
1145	1150	1155	1160
agc tca aat cca agc tct cct gga aga ata aag ggg agg ctt gat agt			3677
Ser Ser Asn Pro Ser Ser Pro Gly Arg Ile Lys Gly Arg Leu Asp Ser			
1165	1170	1175	
tct gaa atg gat cac agt gaa aat gaa gat tac aca atg tct tca cct			3725
Ser Glu Met Asp His Ser Glu Asn Glu Asp Tyr Thr Met Ser Ser Pro			
1180	1185	1190	
ttg ccg ggg aaa aaa agt gac aag aga gac gac tct gat ctt gta agg			3773
Leu Pro Gly Lys Ser Asp Lys Arg Asp Asp Ser Asp Leu Val Arg			
1195	1200	1205	
tct gaa ttg gag aag cct aga ggc agg aaa aaa acg ccc gtc aca gaa			3821
Ser Glu Leu Glu Lys Pro Arg Gly Arg Lys Lys Thr Pro Val Thr Glu			
1210	1215	1220	
cag gag gag aaa tta ggt atg gat gac ttg act aag ttg gta cag gaa			3869
Gln Glu Glu Lys Leu Gly Met Asp Asp Leu Thr Lys Leu Val Gln Glu			
1225	1230	1235	1240
cag aaa cct aaa ggc agt cag cga agt cgg aaa aga ggc cat acg gct			3917
Gln Lys Pro Lys Gly Ser Gln Arg Ser Arg Lys Arg Gly His Thr Ala			
1245	1250	1255	
tca gaa tct gat gaa cag cag tgg cct gag gaa aag agg ctc aaa gaa			3965
Ser Glu Ser Asp Glu Gln Gln Trp Pro Glu Glu Lys Arg Leu Lys Glu			
1260	1265	1270	
gat ata tta gaa aat gaa gat gaa cag aat agt ccg cca aaa aag ggt			4013
Asp Ile Leu Glu Asn Glu Asp Glu Gln Asn Ser Pro Pro Lys Lys Gly			
1275	1280	1285	
aaa aga ggc cga cca cca aaa cct ctt ggt gga ggt aca cca aaa gaa			4061
Lys Arg Gly Arg Pro Pro Lys Pro Leu Gly Gly Thr Pro Lys Glu			
1290	1295	1300	
gag cca aca atg aaa act tct aaa aaa gga agc aaa aaa aaa tct gga			4109
Glu Pro Thr Met Lys Thr Ser Lys Lys Gly Ser Lys Lys Ser Gly			
1305	1310	1315	1320
cct cca gca cca gag gag gaa gaa gaa aga caa agt gga aat			4157
Pro Pro Ala Pro Glu Glu Glu Glu Arg Gln Ser Gly Asn			
1325	1330	1335	
acg gaa cag aag tcc aaa agc aaa cag cac cga gtg tca agg aga gca			4205
Thr Glu Gln Lys Ser Lys Lys Gln His Arg Val Ser Arg Arg Ala			
1340	1345	1350	
cag cag aga gca gaa tct cct gaa tct agt gca att gaa tcc aca cag			4253
Gln Gln Arg Ala Glu Ser Pro Glu Ser Ser Ala Ile Glu Ser Thr Gln			

1355	1360	1365	
tcc aca cca cag aaa gga	cga gga aga cca tca aaa acg cca tca cca		4301
Ser Thr Pro Gln Lys Gly	Arg Gly Arg Pro Ser Lys Thr Pro Ser Pro		
1370	1375	1380	
tca caa cca aaa aaa aat gtg	taagttgtaa atattacatt tcaaaccatat		4352
Ser Gln Pro Lys Lys Asn Val			
1385	1390		
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ccatatattt agccccatta cactaggta cgc当地ggc当地aaag tgctaaaagg gaacggcgat			4472
gaacaaatgt aattaataac ttctctgtg aaagcttgg aaaaatctt tttttttt			4532
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aagagtggac agttggacct tactttggc accccataca ttgtggta catgcttag			4652
ccatacacat ggtaacattt actatggagt ctgtgaaag tgtaatgtgc gatggctatg			4712
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gaagtgc当地ttg tatagcttt atctgc当地gt ttaaactgac agtacccgac tgtttattgg			4832
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tgtactgaat tctttatccc attttatcat ctttc当地atctt tttatataatc tactgtatca			5312
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<220>
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18

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: motif

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